

Supplementary Table 1. Number of study subjects.

Supplementary Table 1a,1b. Number of individuals for 610 Quad and OmniExpress platform.

Dataset	Platform	Individuals genotyped
AS cases	610 Quad	968
Anhui controls	610 Quad	1227
Shandong controls	660 Quad	685
Guangdong controls	610 Quad	1025
Singapore Chinese controls I	610 Quad	931
Singapore Chinese controls II	610 Quad	1146

Dataset	Platform	Individuals genotyped
AS cases	OmniExpress	997
Shandong controls	OmniZhonghua	1597
Nanjing,Guangzhou controls	OmniExpress	1584
Singapore Chinese controls III	OmniZhonghua	1284

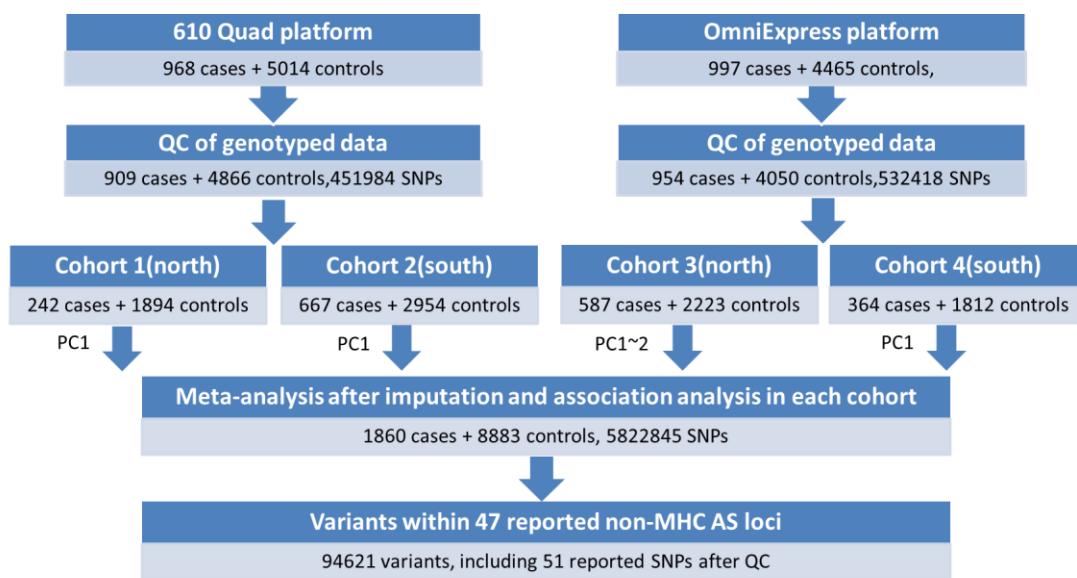
Supplementary Table 1c. Number of individuals of 4 cohorts in final meta-analysis.

Totally 1,860 cases and 8,883 controls are included in meta-analysis from 4 cohorts.

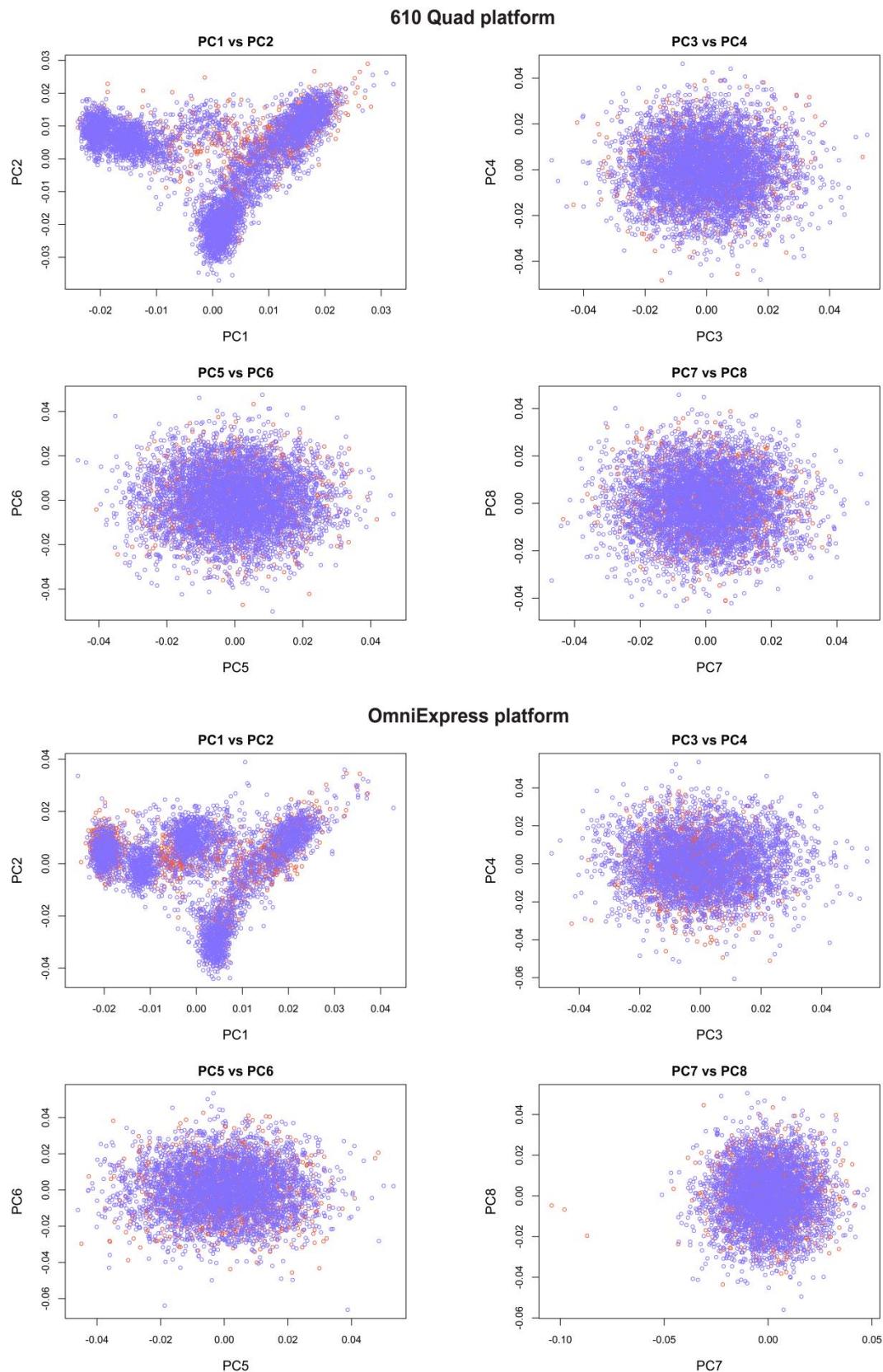
Cohort	platform	Number of cases	Number of controls
Cohort 1	610 Quad	242	1,894 PC1
Cohort 2	610 Quad	667	2,954 PC1
Cohort 3	OmniExpress	587	2,223 PC1-2
Cohort 4	OmniExpress	364	1,812 PC1
Summary	-	1,860	8,883

Supplementary Figure 1. Flowchart of study design and data analysis.

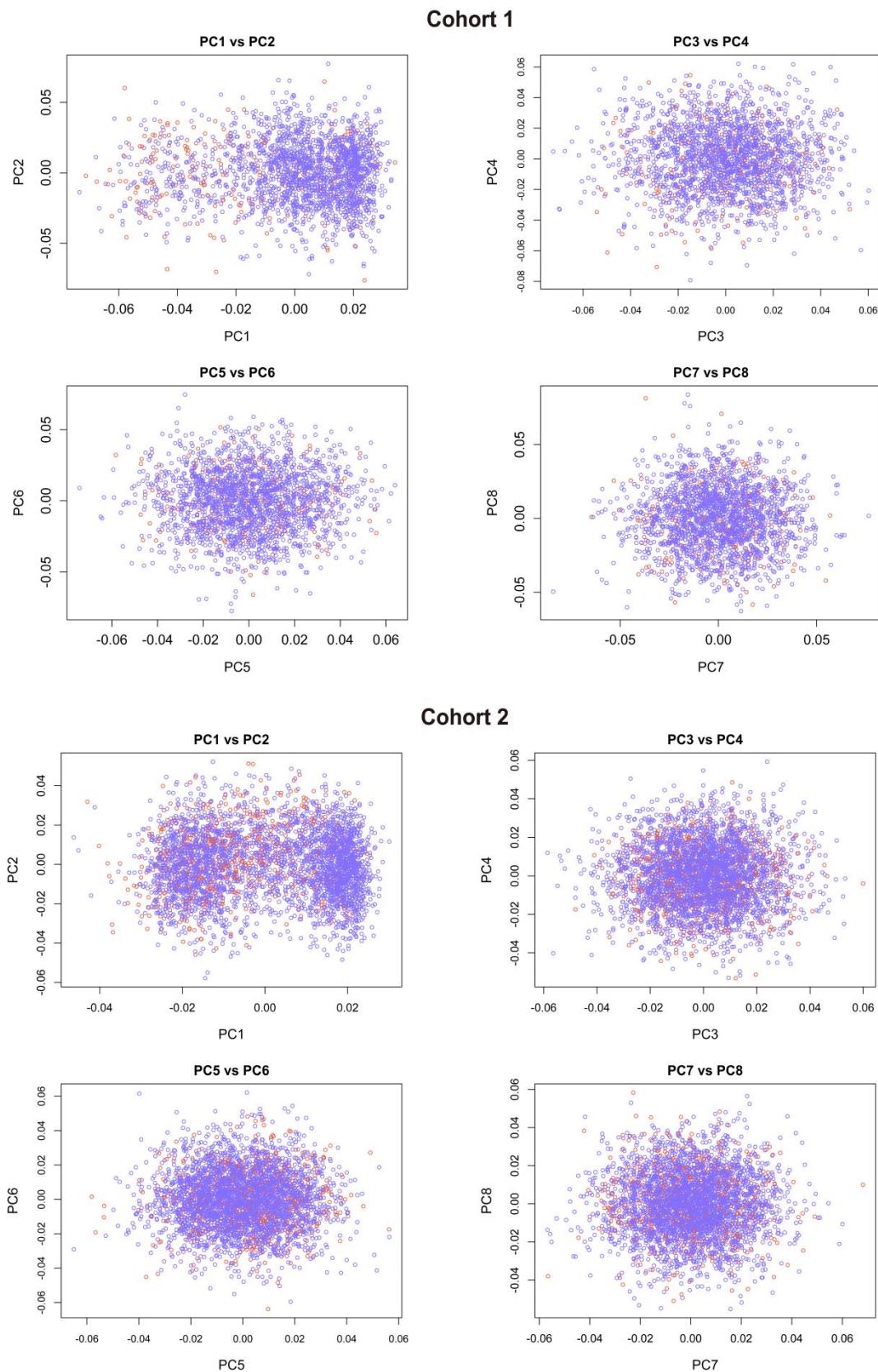
Originally 5,014 controls and 4,465 controls were included for 968 AS cases generated by 610 Quad platform and 997 AS cases by OmniExpress platform, respectively. After stringent QC, 909 cases vs. 4,866 controls and 954 cases vs. 4,050 controls were used for further PCA analysis. Cohort 1 and 3 represented north Chinese population according to PCA and recruitment region of GWAS dataset, while cohort 2 and 4 mainly from south region. In the association analysis PC 1 was used as covariate in cohort 1, 2 and 4, while PC 1 and PC 2 were used in cohort 3. Final meta-analysis result consisted of 1,860 AS cases and 8,883 controls with 5,822,845 non-MHC variants. Totally 94,621 variants within 47 non-MHC AS loci were extracted.



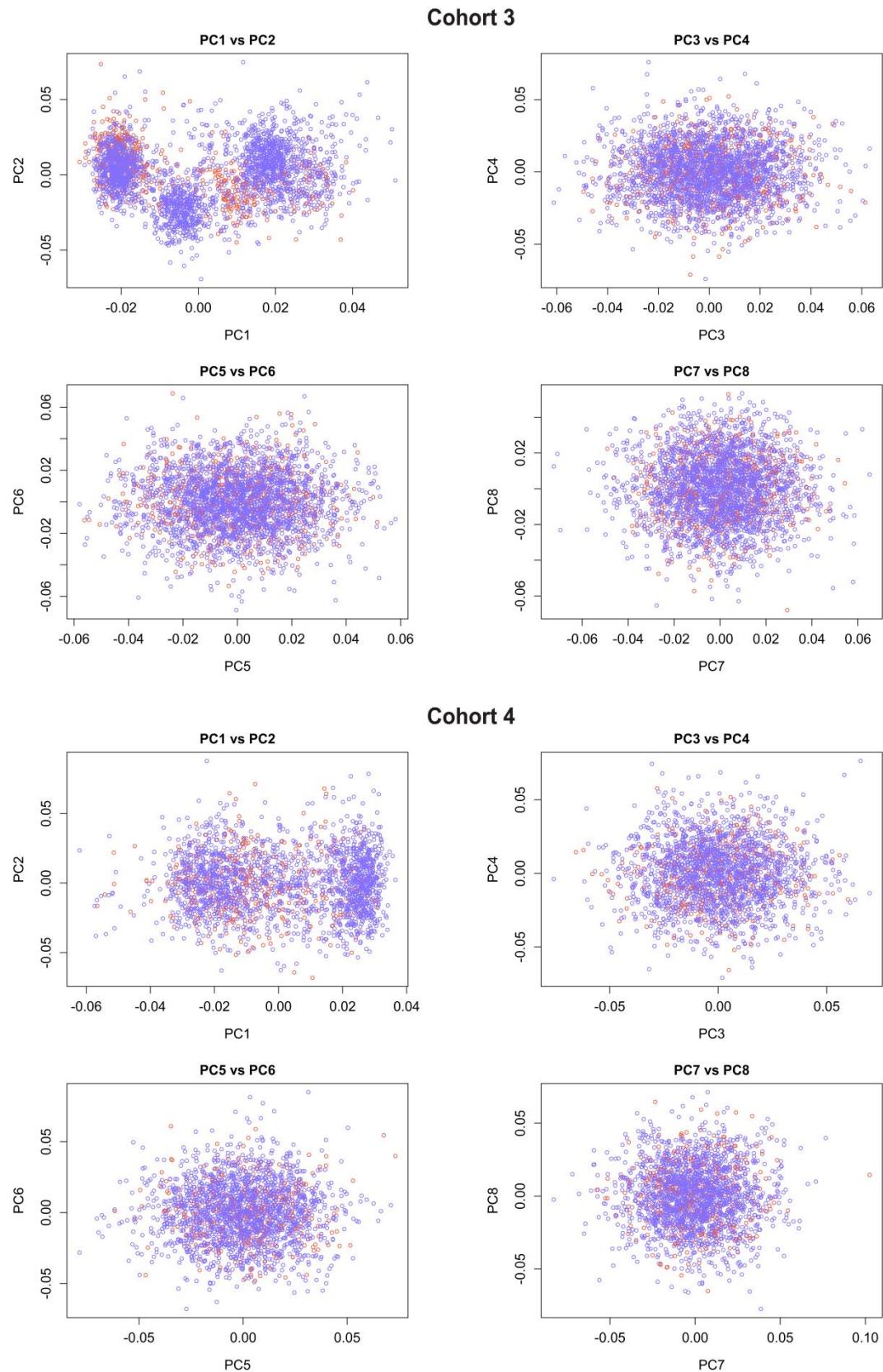
Supplementary Figure 2A. Principal Component Analysis(PCA) plots of samples in two genotyped platforms and four cohorts of north and south China.
Red points: case samples, blue points: control samples.



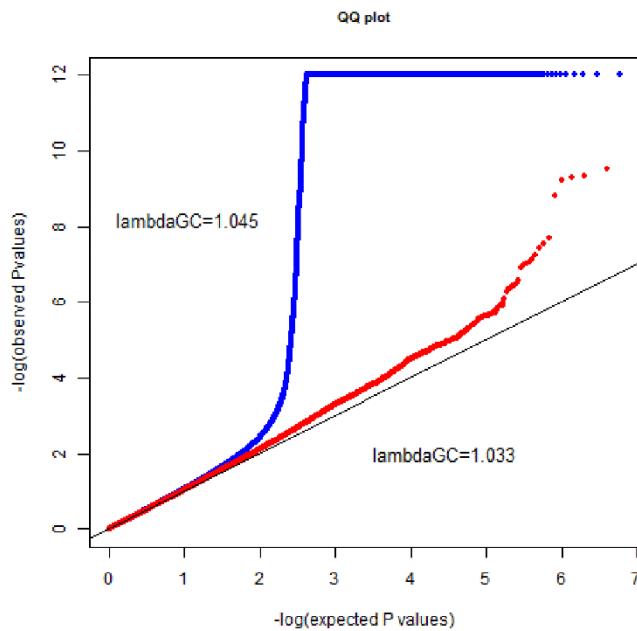
Supplementary Figure 2B. Principal Component Analysis(PCA) plots of samples in two genotyped platforms and four cohorts of north and south China.



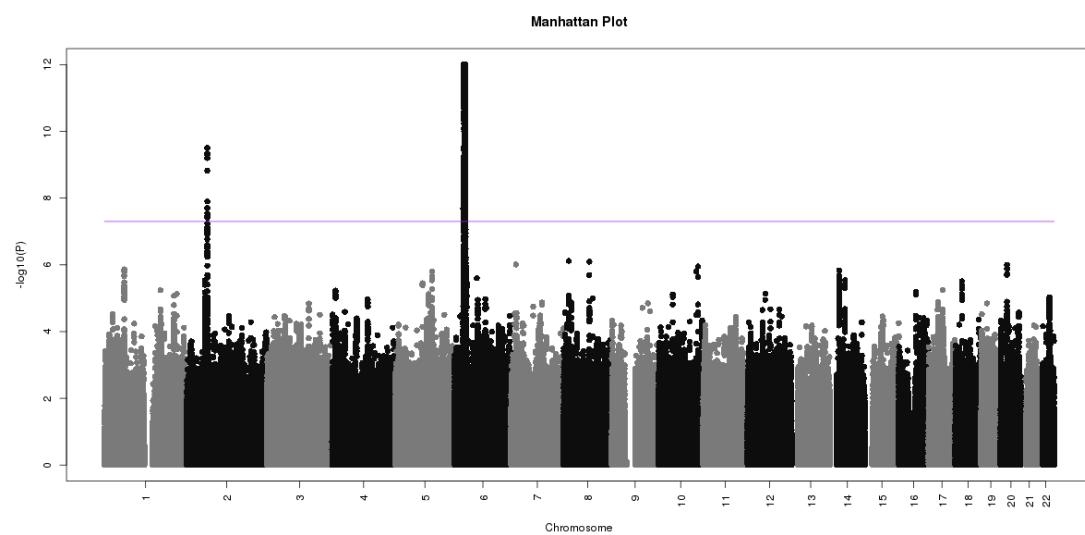
Supplementary Figure 2C. Principal Component Analysis(PCA) plots of samples in two genotyped platforms and four cohorts of north and south China.



Supplementary Figure 3. Quantile-Quantile plot (a) of observed P values and Manhattan plot (b) for whole-genome associations.



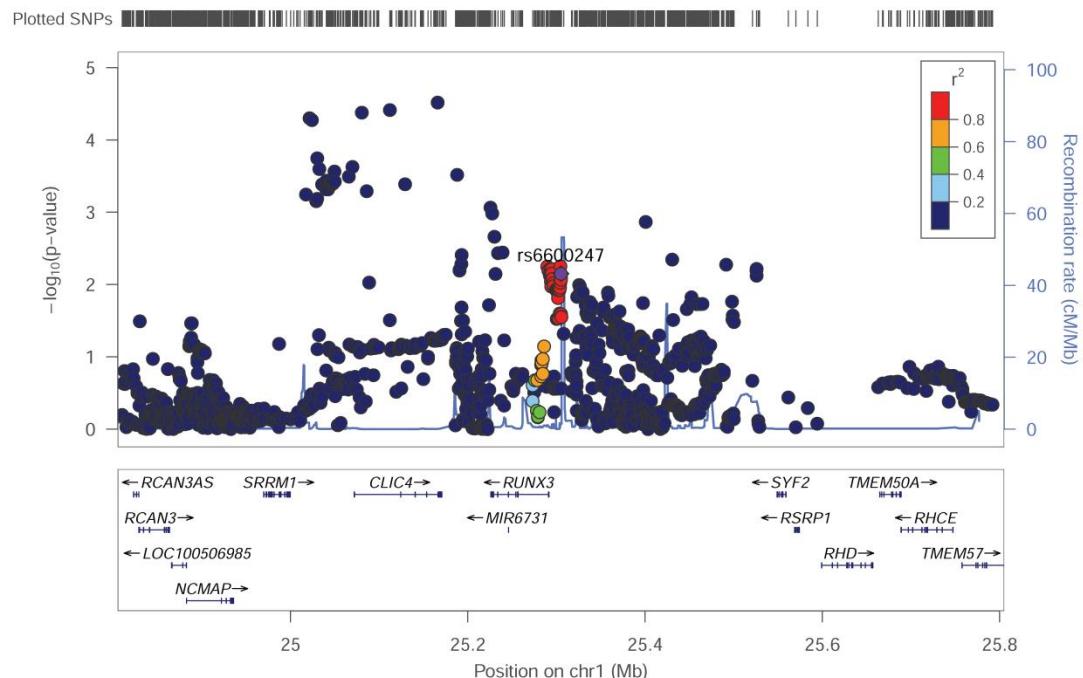
(a) Q-Q plot. Blue points represent MHC variants and red points stand for non-MHC variants.



(b) Manhattan plot for whole-genome associations signals of meta-analysis results. The points within MHC region with P value <10⁻¹² were truncated. Purple line: -log₁₀(5×10⁻⁸).

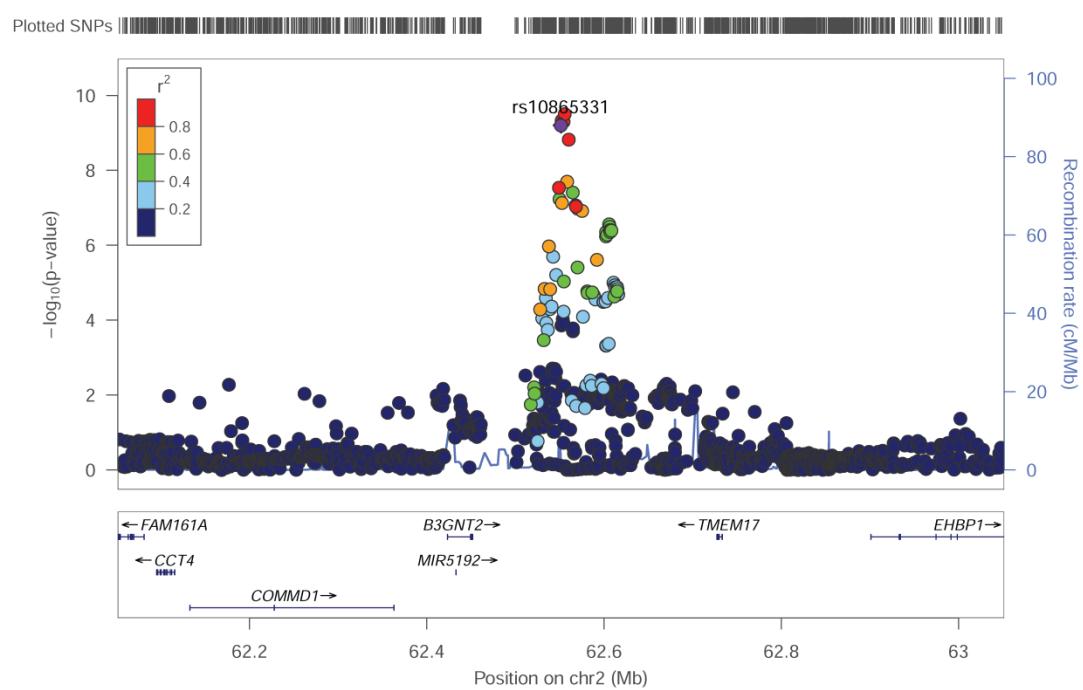
Supplementary Figure 4. Regional association plots and linkage disequilibrium patterns with the 16 AS-associated SNPs in 13 reported non-MHC loci. The reported SNP (labeled by rsID) is shown in purple, and its LD (r^2) with the remaining SNPs is indicated by color.

rs6600247



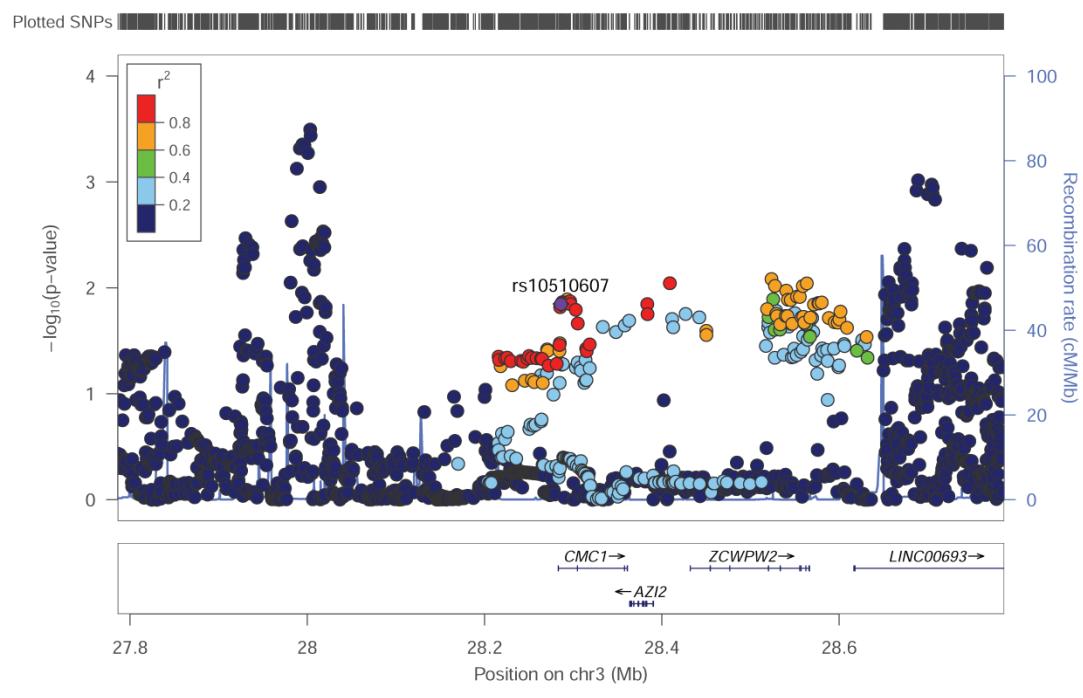
(a) rs6600247

rs10865331



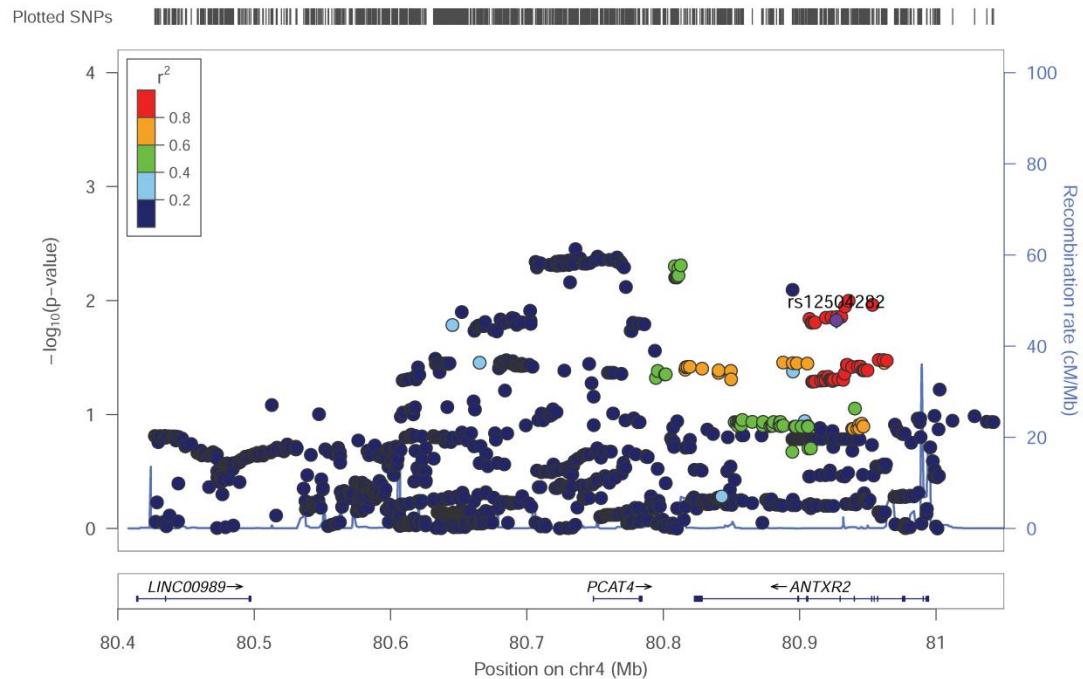
(b) rs10865331

rs10510607



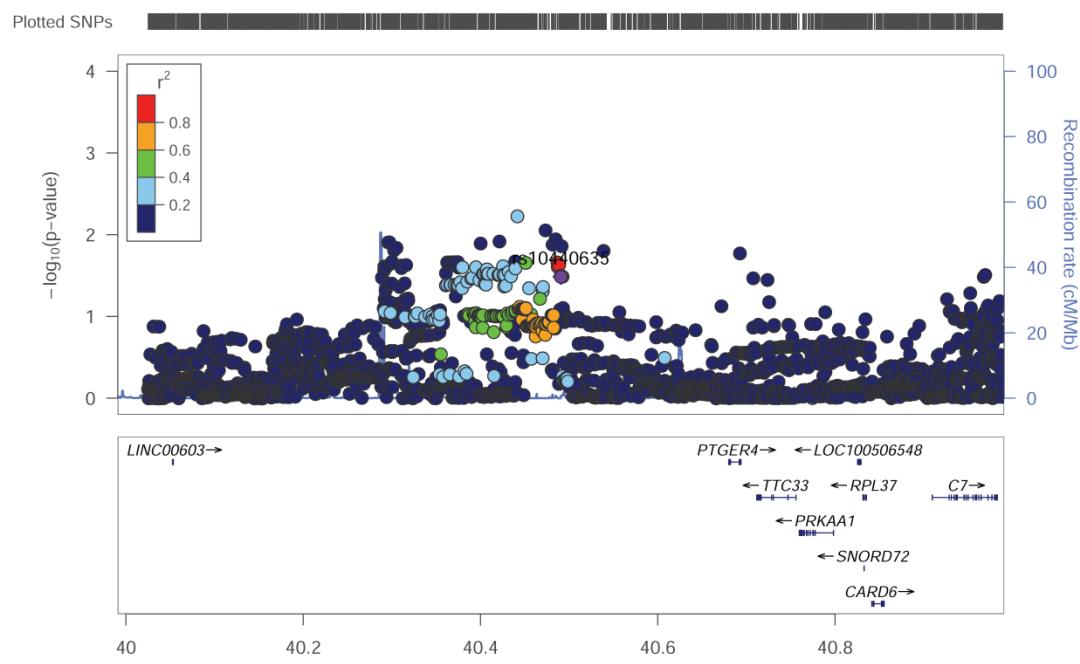
(c) rs10510607

rs12504282

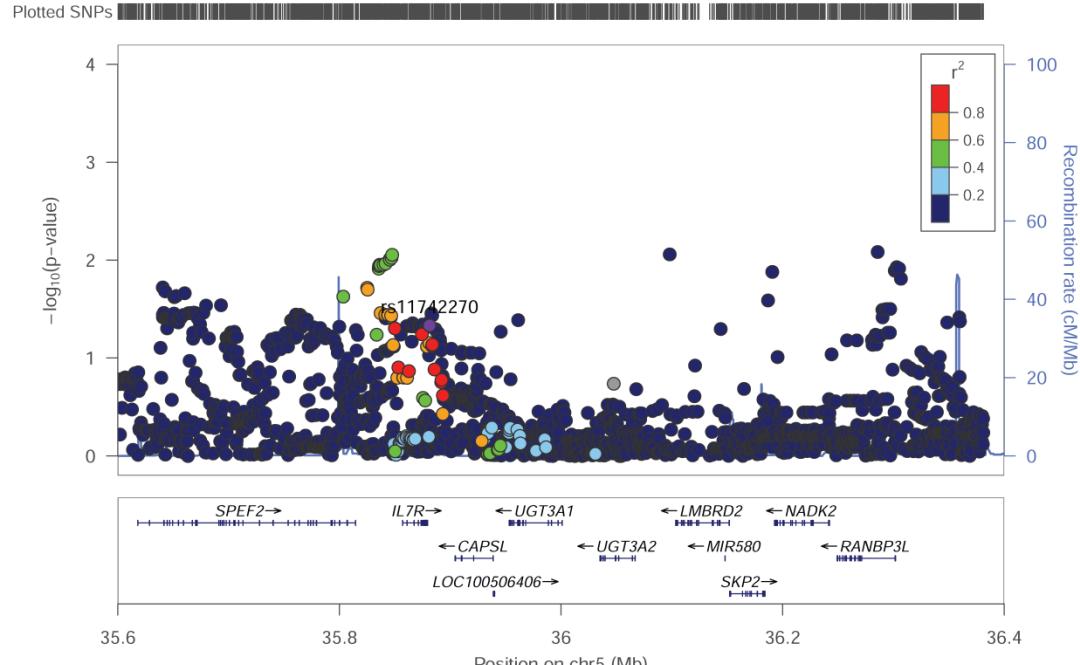


(d) rs12504282

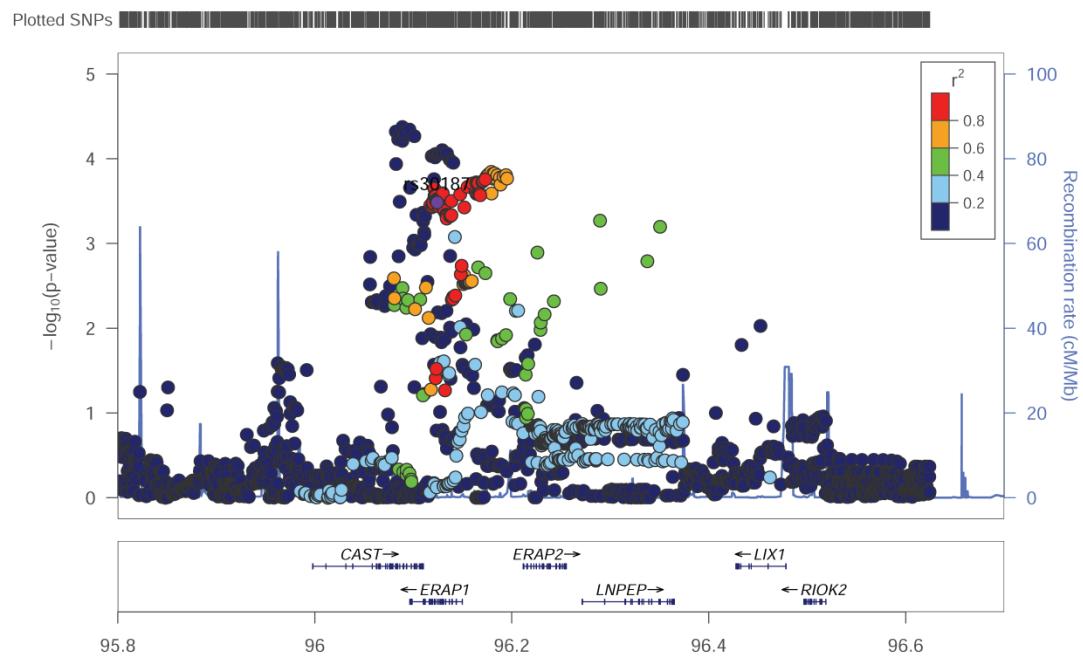
rs10440635



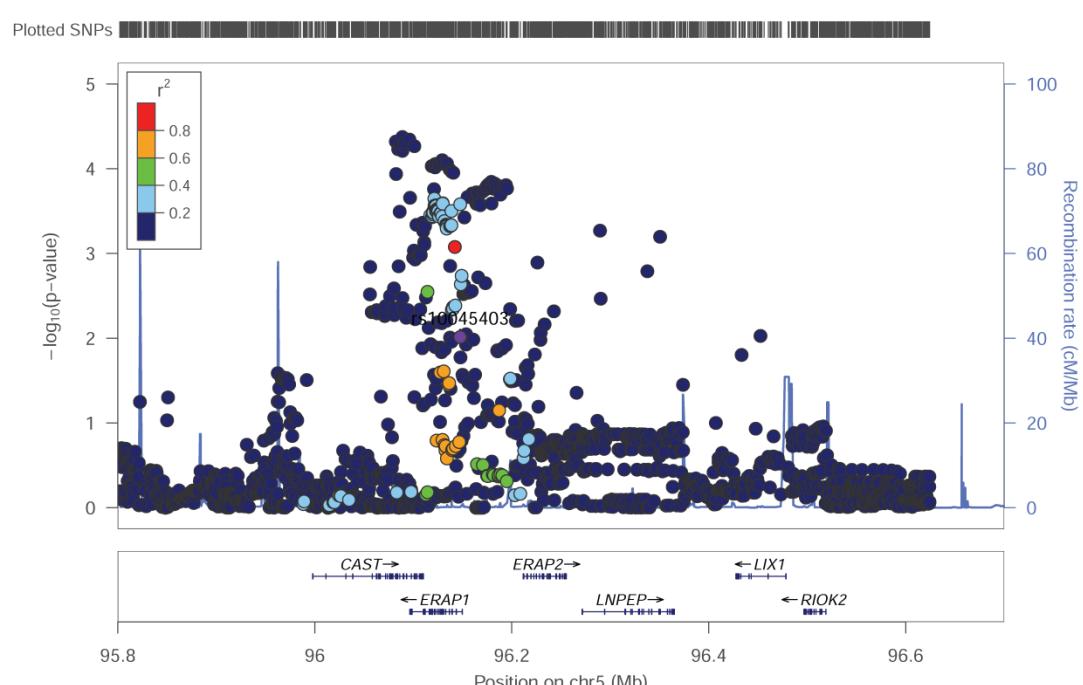
rs11742270



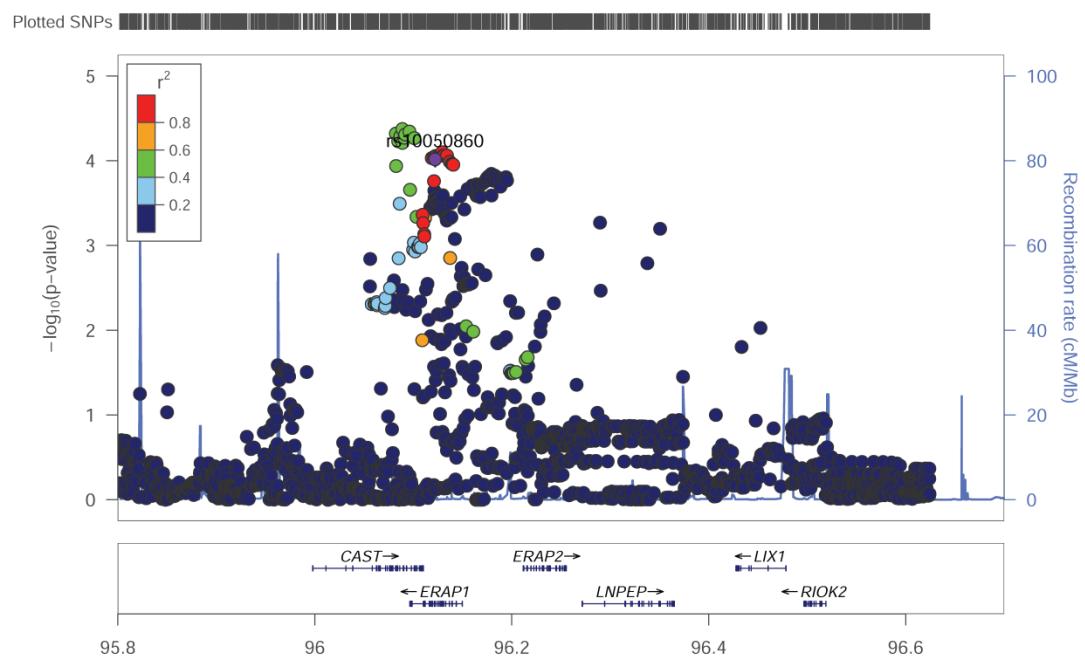
rs30187



rs10045403

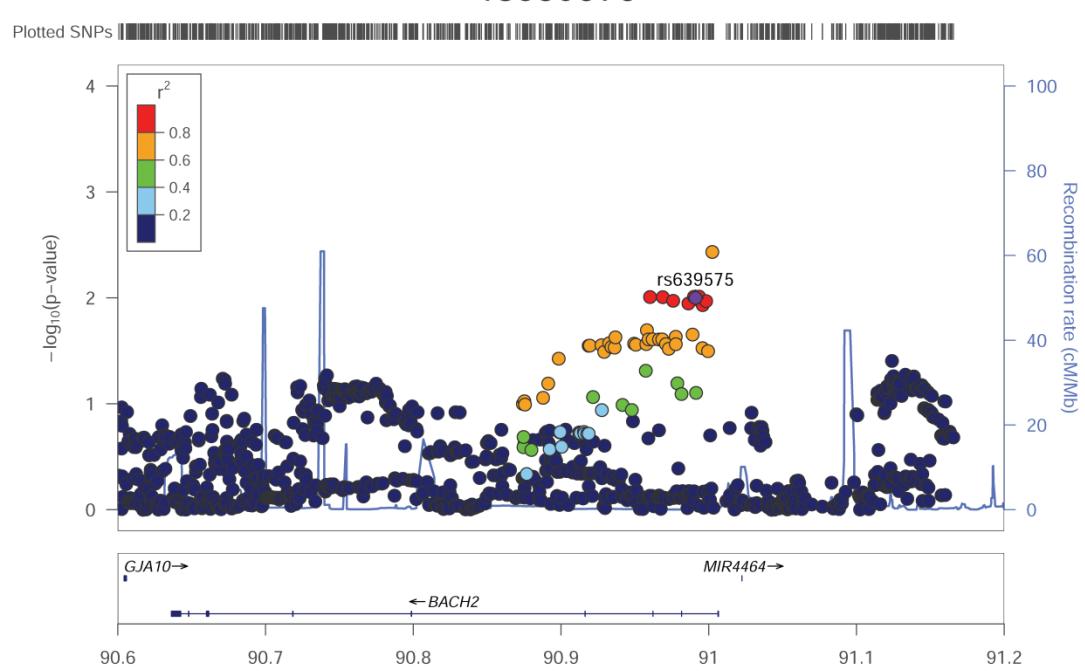


rs10050860



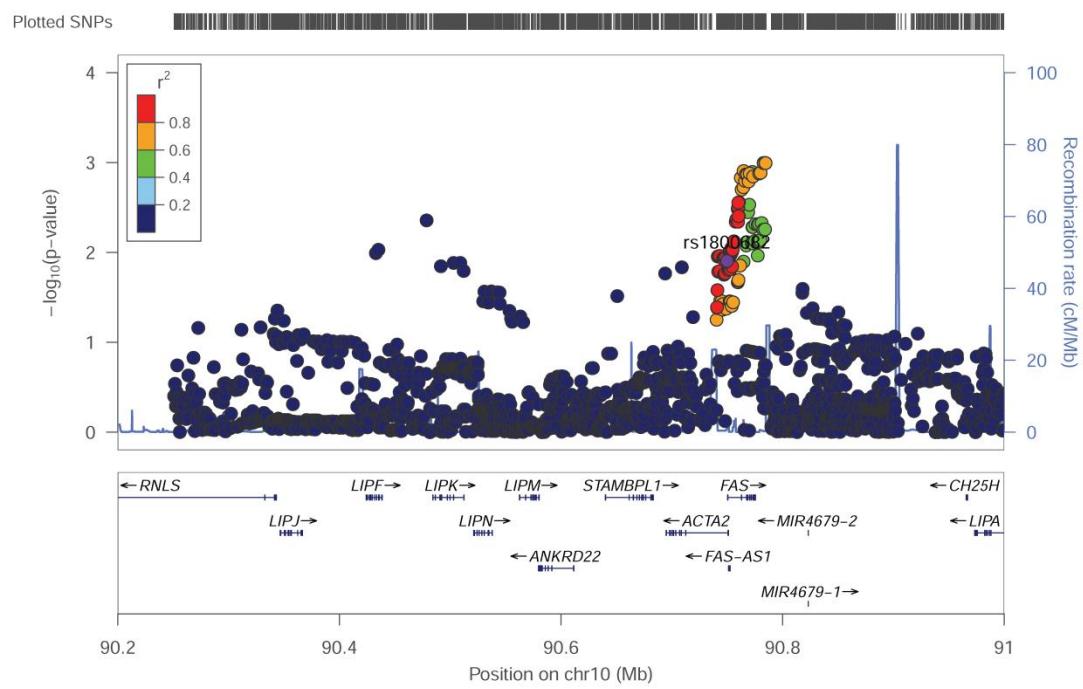
(i) rs10050860

rs639575

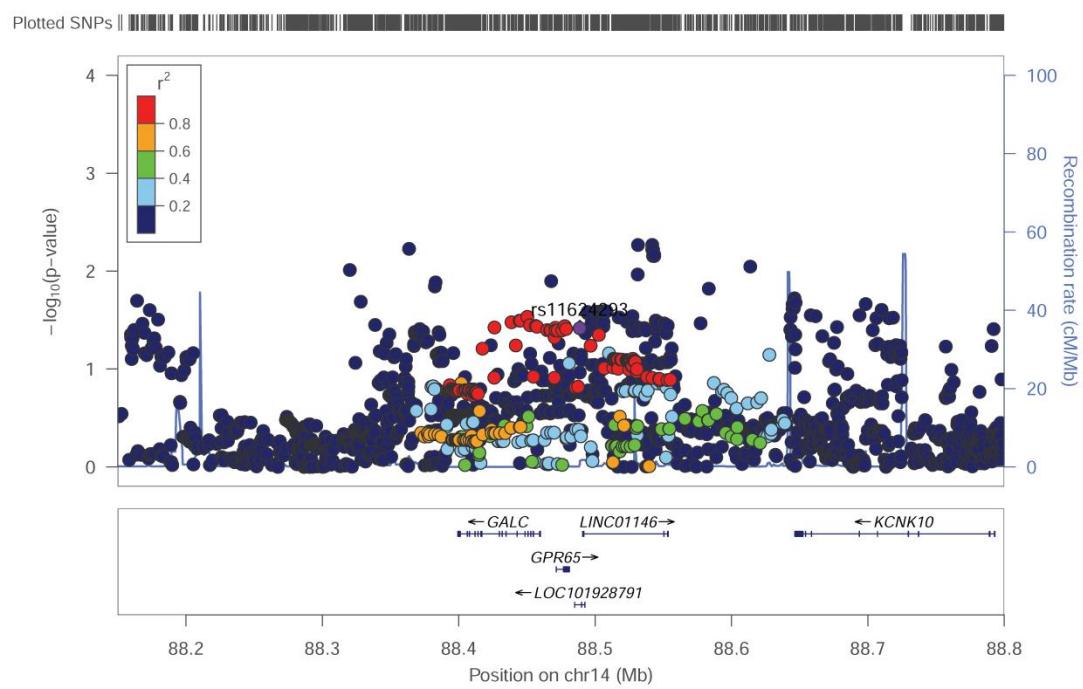


(j) rs639575

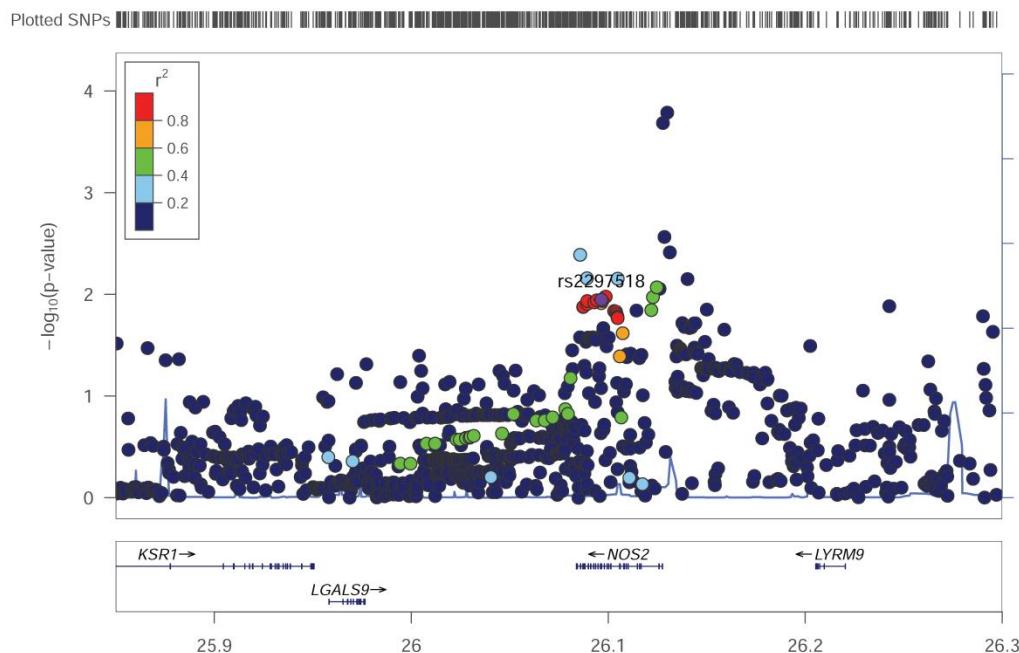
rs1800682



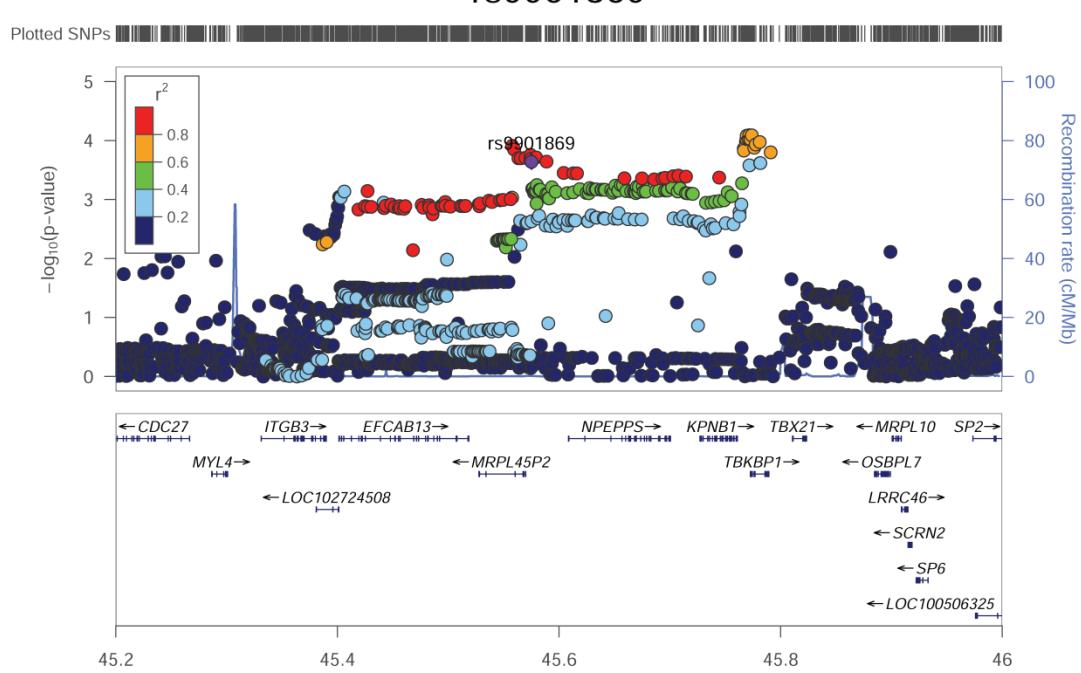
rs11624293



rs2297518

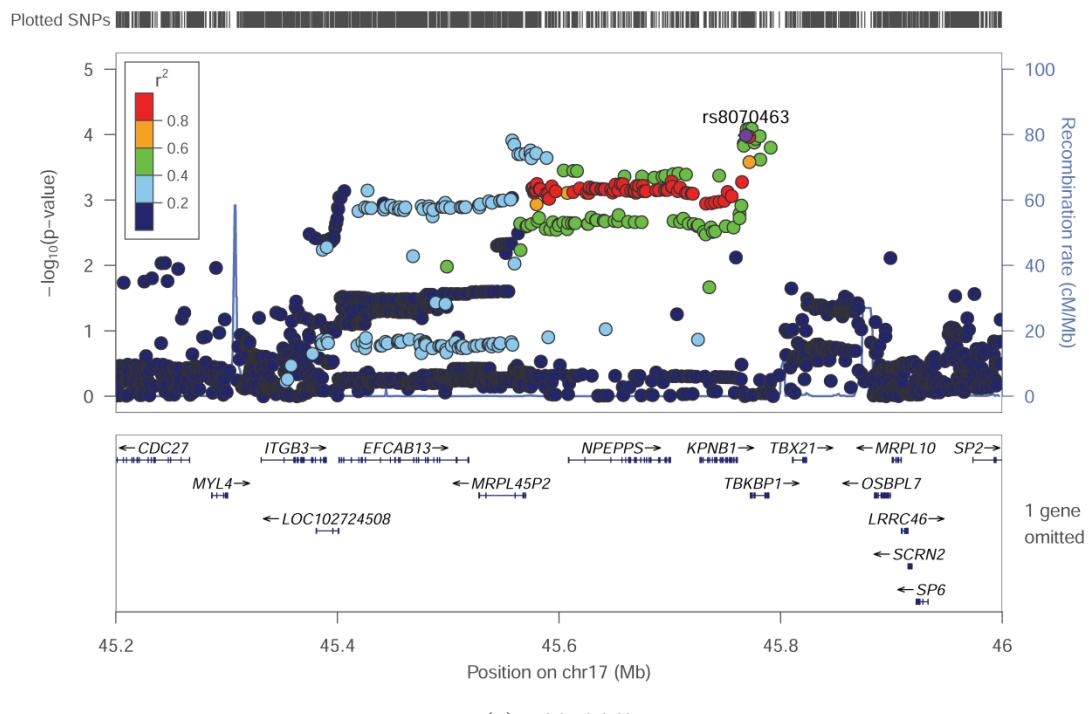


rs9901869

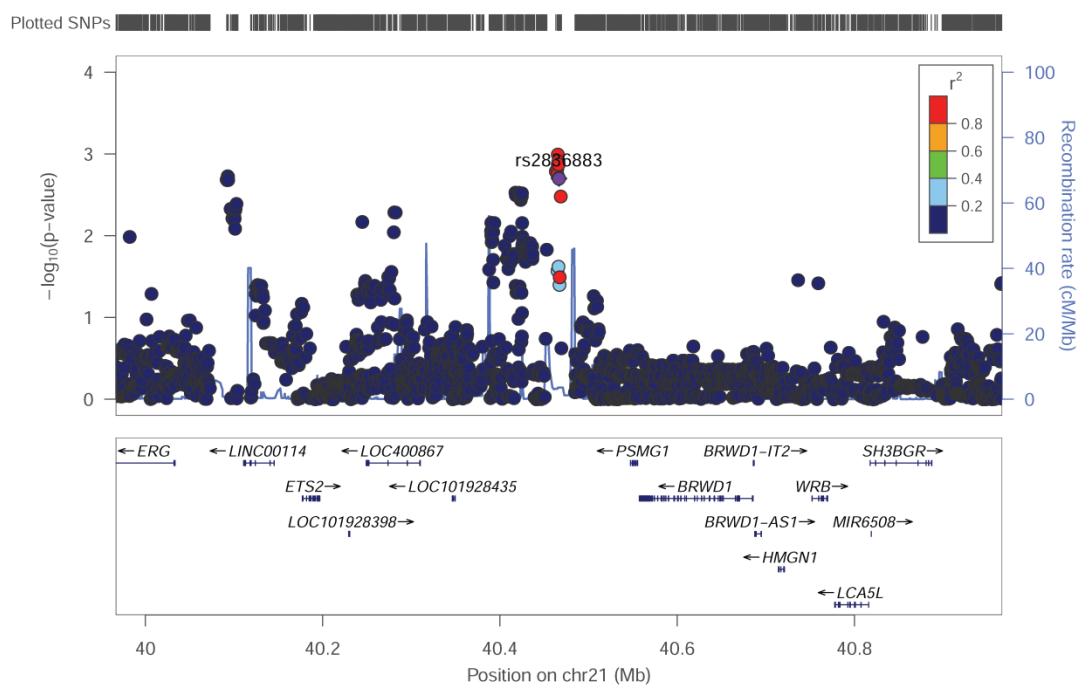


(n) rs9901869

rs8070463



rs2836883



Supplementary Table 2. Association results of 64 reported SNPs with AS susceptibility across Europeans and Chinese Han

Locus	SNP	Position (Build 37)	Nearby Gene(s)	A1/A2	Europeans		Chinese Han				Power
					OR	P	OR(95%CI)	P	P_het	I ²	
1p31	rs11209026	67705958	IL23R	G/A	1.65 ^c	6.0×10 ⁻²⁸	-	-	-	-	-
1p31	rs12141575	67747436	IL23R	A/G	1.15 ^c	9.4×10 ⁻¹¹	1.05(0.97~1.13)	2.25×10 ⁻¹	0.56	0	95.20%
1p36	rs6600247	25305114	RUNX3	C/T	1.16 ^c	1.3×10 ⁻¹⁴	1.12(1.03~1.21)	7.08×10 ⁻³	0.6	0	92.50%
1p36	rs11249215	25297184	RUNX3	A/G	1.17 ^b	9.2×10 ⁻¹¹	-	-	-	-	-
1q21	rs4129267	154426264	IL6R	C/T	1.18 ^c	2.1×10 ⁻¹⁵	1.04(0.97~1.12)	2.84×10 ⁻¹	0.74	0	98.10%
1q23	rs1801274	161479745	FCGR2A-ITLN1	A/G	1.12 ^c	9.9×10 ⁻¹⁰	1.03(0.95~1.11)	4.79×10 ⁻¹	0.26	25.4	79.10%
1q23	rs2039415	160854445	FCGR2A-ITLN1	C/T	1.11 ^e	3.9×10 ⁻⁸	1.02(0.94~1.11)	6.01×10 ⁻¹	0.7	0	70.90%
1q32	rs41299637	200877850	GPR25-KIF21B	T/G	1.20 ^c	7.0×10 ⁻¹⁶	-	-	-	-	-
1q32	rs12758027	210794808	HHAT	C/T	1.09 ^c	6.0×10 ⁻⁶	-	-	-	-	-
2p15	rs10865331	62551472	Intergenic	A/G	1.34 ^b	6.5×10 ⁻³⁴	1.26(1.17~1.35)	6.30×10 ⁻¹⁰	0.08	55.1	100.00%
2p25	rs2666218	9402988	ASAP2	G/A	1.12 ^e	2.0×10 ⁻⁸	1.07(0.98~1.18)	1.46×10 ⁻¹	0.93	0	67.10%
2q11	rs4851529	102647300	IL1R2-IL1R1	G/A	1.10 ^c	1.0×10 ⁻⁶	1.05(0.97~1.13)	2.07×10 ⁻¹	0.08	55.7	71.60%
2q11	rs2310173	102663628	IL1R2	T/G	1.17 ^a	4.8×10 ⁻⁷	-	-	-	-	-
2q11	rs2192752	102769373	IL1R2-IL1R1	G/T	1.11 ^c	4.1×10 ⁻⁶	1.02(0.92~1.12)	7.69×10 ⁻¹	0.77	0	50.50%
2q31	rs12615545	182048452	UBE2E3	C/T	1.11 ^c	2.3×10 ⁻⁷	1.04(0.96~1.12)	3.00×10 ⁻¹	0.88	0	72.40%
2q33	rs11306716	204707771	-	I/D	1.14 ^e	1.3×10 ⁻¹³	-	-	-	-	-
2q37	rs4676410	241563739	GPR35	A/G	1.13 ^c	2.1×10 ⁻⁷	1.07(0.99~1.16)	8.63×10 ⁻²	0.01	73.4	86.00%
3p24	rs13093489	27794907	EOMES	A/C	1.12 ^c	1.1×10 ⁻⁷	1.07(1~1.15)	6.41×10 ⁻²	0.98	0	84.70%
3p24	rs10510607	28286261	CMC1	C/T	1.15 ^e	2.3×10 ⁻⁸	1.1(1.02~1.18)	1.42×10 ⁻²	0.27	22.7	94.90%
3q22	rs6781808	137441372	NPM1P17	C/T	1.14 ^e	4.2×10 ⁻¹⁰	1.1(0.99~1.23)	8.10×10 ⁻²	0.89	0	59.10%
4q21	rs12504282	80927001	ANTXR2	T/C	1.14 ^d	6.7×10 ⁻⁹	1.18(1.03~1.34)	1.49×10 ⁻²	0.87	0	46.00%
4q24	rs3774937	103434253	NF-KB1	C/T	1.12 ^e	7.8×10 ⁻¹⁰	1.05(0.97~1.13)	2.18×10 ⁻¹	0.48	0	82.90%
5p13	rs12186979	40524860	PTGER4	G/A	1.09 ^c	5.4×10 ⁻⁶	1.06(0.97~1.17)	2.14×10 ⁻¹	0.39	1.3	45.00%

5p13	rs10440635	40490790	PTGER4	A/G	1.13 ^b	2.6×10^{-7}		1.1(1.01~1.2)	3.26×10^{-2}	0.37	5.5	78.00%
5p13	rs11742270	35881443	IL7R	G/A	1.11 ^c	1.9×10^{-6}		1.11(1~1.22)	4.63×10^{-2}	0.42	0	48.90%
5p15	rs11750385	10521668	RP11-1C1.5	G/T	1.11 ^c	2.3×10^{-9}		-	-	-	-	-
5q15	rs30187	96124330	ERAP1	T/C	1.32 ^c	1.3×10^{-41}		1.14(1.06~1.23)	3.27×10^{-4}	0.72	0	100.00%
5q15	rs10045403	96147733	ERAP1	A/G	1.20 ^c	5.8×10^{-14}		1.14(1.03~1.26)	9.65×10^{-3}	0.67	0	91.40%
5q15	rs10050860	96122210	ERAP1	C/T	1.18 ^b	1.9×10^{-7}		1.42(1.19~1.69)	$4.09 \times 10^{-5^*}$	0.47	0	39.80%
5q15	rs2910686	96252589	ERAP1-ERAP2	C/T	1.17 ^c	4.5×10^{-17}		1.05(0.98~1.13)	1.95×10^{-1}	0.88	0	97.40%
5q33	rs6871626	158826792	IL12B	A/C	1.12 ^c	6.0×10^{-8}		-	-	-	-	-
5q33	rs6556416	158818745	IL12B	C/A	1.16 ^b	1.9×10^{-8}		1.1(0.97~1.25)	1.32×10^{-1}	0.37	5.6	57.10%
6p22	rs6908425	20728731	CDKAL1	C/T	1.15 ^e	8.5×10^{-10}		1.01(0.91~1.11)	9.08×10^{-1}	0.25	27.8	83.30%
6q15	rs17765610	90665773	BACH2	G/A	1.17 ^c	3.3×10^{-8}		1.14(0.86~1.49)	3.63×10^{-1}	0.81	0	22.50%
6q15	rs639575	90991131	BACH2	T/A	1.08 ^c	8.6×10^{-5}		1.1(1.02~1.18)	9.99×10^{-3}	0.48	0	54.00%
6q27	rs67025039	167415405	FGFR1OP	I/D	1.21 ^e	3.3×10^{-26}		-	-	-	-	-
7p21	rs1525735	17197571	-	C/T	1.12 ^e	4.6×10^{-10}		1.06(0.95~1.18)	2.89×10^{-1}	0.92	0	57.00%
7q31	rs2402752	124439599	GPR37	T/C	1.11 ^c	2.4×10^{-6}		1.04(0.96~1.13)	2.95×10^{-1}	0.16	42.1	68.40%
9q34	rs1128905	139253839	CARD9	C/T	1.12 ^c	1.6×10^{-9}		1.03(0.95~1.11)	4.93×10^{-1}	0.63	0	77.30%
9q34	rs10781500	139269338	CARD9	T/C	1.12 ^b	1.1×10^{-6}		1.01(0.94~1.1)	7.20×10^{-1}	0.39	0.6	75.60%
10q22	rs1250550	81060317	ZMIZ1	A/C	1.11 ^c	5.8×10^{-7}		1.08(1~1.16)	5.29×10^{-2}	1	0	76.50%
10q23	rs1800682	90749963	ACTA2	A/G	1.12 ^e	2.1×10^{-10}		1.1(1.02~1.18)	1.24×10^{-2}	0.21	33.7	83.50%
10q24	rs11190133	101278725	NKX2-3	C/T	1.18 ^c	1.7×10^{-14}		1.03(0.96~1.11)	3.91×10^{-1}	0.46	0	98.50%
11q24	rs7933433	128194450	-	T/G	1.12 ^e	2.6×10^{-9}		1.06(0.98~1.15)	1.17×10^{-1}	0.88	0	82.10%
12p13	rs1860545	6446777	LTBR-TNFRSF1A	G/A	1.13 ^c	8.3×10^{-10}		1.06(0.95~1.19)	2.93×10^{-1}	0.08	55.6	50.40%
12p13	rs7954567	6491125	LTBR-TNFRSF1A	A/G	1.11 ^c	1.2×10^{-7}		-	-	-	-	-
12p13	rs11616188	6502742	LTBR-TNFRSF1A	A/G	1.19 ^b	4.1×10^{-12}		1.06(0.86~1.31)	5.67×10^{-1}	0.31	16.1	40.00%
12q24	rs11065898	111862575	SH2B3	T/C	1.13 ^c	1.7×10^{-7}		1.03(0.96~1.11)	4.26×10^{-1}	0.69	0	86.90%
14q13	rs8006884	35563211	PPP2R3C	C/T	1.11 ^e	3.2×10^{-8}		1.07(0.99~1.15)	7.77×10^{-2}	0.56	0	78.10%

14q31	rs11624293	88488821	GPR65	C/T	1.23 ^c	1.8×10^{-7}		1.11(1.01~1.23)	3.82×10^{-2}	0.02	69.6	98.20%
16p11	rs75301646	28617885	IL27-SULT1A1	A/G	1.11 ^c	1.4×10^{-7}		-	-	-	-	-
16p11	rs34670647	30171017	-	D/T	1.23 ^e	1.3×10^{-31}		-	-	-	-	-
17q11	rs2531875	26148167	NOS2	G/T	1.12 ^c	1.3×10^{-8}		1.09(1~1.18)	5.44×10^{-2}	0.39	0.9	76.40%
17q11	rs2297518	26096597	NOS2	A/G	1.13 ^c	6.3×10^{-7}		1.14(1.03~1.26)	1.13×10^{-2}	0.1	52.9	68.10%
17q21	rs9901869	45575206	NPEPPS-TBKBP1	A/G	1.15 ^c	2.3×10^{-12}		1.15(1.07~1.24)	2.29×10^{-4}	0.48	0	93.30%
17q21	rs8070463	45768836	NPEPPS-TBKBP1	C/T	1.14 ^b	5.3×10^{-8}		1.16(1.08~1.25)	1.03×10^{-4}	0.41	0	92.80%
17q23	rs196941	62147192	ERN1	G/C	1.14 ^e	4.0×10^{-11}		1.02(0.94~1.1)	6.86×10^{-1}	0.47	0	91.60%
18p11	rs45450798	12792940	PTPN2	G/C	1.14 ^e	3.0×10^{-8}		1.06(0.97~1.17)	2.16×10^{-1}	0.03	66	79.50%
19p13	rs35164067	10525181	TYK2	G/A	1.16 ^c	6.5×10^{-9}		1.05(0.97~1.13)	2.28×10^{-1}	0.4	0	97.10%
19p13	rs6511701	10625067	TYK2	A/C	1.10 ^c	1.4×10^{-4}		-	-	-	-	-
21q22	rs2836883	40466744	Intergenic	G/A	1.19 ^c	1.8×10^{-14}		1.16(1.06~1.28)	2.00×10^{-3}	0.56	0	90.20%
21q22	rs7282490	45615741	ICOSLG	G/A	1.10 ^c	1.4×10^{-6}		1.01(0.94~1.09)	7.29×10^{-1}	0.5	0	71.00%
22q11	rs2283790	21956653	UBE2L3	G/A	1.12 ^c	1.2×10^{-6}		1.02(0.95~1.1)	6.21×10^{-1}	0.79	0	84.50%
22q13	rs1569414	45727565	FAM118A	T/G	1.15 ^e	2.9×10^{-11}		1.06(0.98~1.14)	1.26×10^{-1}	0.43	0	95.20%

-: Data not available. A1:risk allele,A2:non-risk allele. RAF: risk allele frequency. P_{het} : *p*-value for the heterogeneity test. Power: detection power in our dataset based on the reported odds ratios (ORs) of published GWAS in Europeans. *: Fisher's exact test. ^a: 2010 AS GWAS comprising of 2951cases and 6658controls; ^b: 2011 AS GWAS comprising of 5134cases and 13262controls; ^c: 2013 AS GWAS comprising of 9069cases and 13578controls; ^d: 2014 AS GWAS comprising of 6001cases and 17506controls; ^e: 2016 AS GWAS comprising of 9069cases and 34213controls.

Supplementary Table 3A. Potential non-MHC variants within reported loci. Other potential non-MHC associations ($P<5.0\times10^{-4}$) within reported AS susceptibility loci in Chinese Han.

Locus	Lead SNP	Position (Build 37)	Nearby Genes	A1/A2	RAF(Case/control) in 4 cohorts				OR(95%CI)	P	P_het	I ²
Common variants												
1p36	rs12030164	25166082	RUNX3-CLIC4	A/G	0.15/0.12	0.17/0.14	0.15/0.13	0.16/0.15	1.26(1.13~1.40)	3.03×10^{-5}	0.84	0.0
1q32	rs650854	210465315	HHAT	G/C	0.46/0.41	0.40/0.37	0.43/0.40	0.42/0.37	1.19(1.10~1.29)	8.43×10^{-6}	0.27	22.8
2p15	rs13024541	62555737	Intergenic	T/C	0.46/0.41	0.60/0.52	0.49/0.42	0.58/0.53	1.27(1.18~1.36)	3.12×10^{-10}	0.10	51.5
2q11	rs2041751	102698360	IL1R2-IL1R1	G/A	0.20/0.21	0.19/0.18	0.22/0.20	0.23/0.17	1.19(1.08~1.31)	2.65×10^{-4}	0.17	39.8
2q33.2	rs12990568	204633655	-	T/A	0.53/0.54	0.57/0.55	0.56/0.51	0.58/0.54	1.15(1.07~1.24)	2.49×10^{-4}	0.32	13.7
2q37	rs10153794	241215701	GPR35	A/G	0.42/0.44	0.45/0.40	0.45/0.42	0.43/0.39	1.15(1.07~1.24)	1.70×10^{-4}	0.22	31.4
3p24.1	rs3905899	28003439	CMC1	C/G	0.39/0.34	0.31/0.28	0.36/0.33	0.32/0.29	1.16(1.07~1.25)	3.20×10^{-4}	0.58	0.0
5q15	rs17401719	96089046	ERAP1	T/C	0.92/0.91	0.93/0.92	0.94/0.91	0.94/0.92	1.32(1.15~1.50)	4.21×10^{-5}	0.54	0.0
6q27	rs86757	167507676	FGFR1OP	T/C	0.11/0.09	0.14/0.10	0.12/0.11	0.12/0.10	1.28(1.14~1.44)	3.40×10^{-5}	0.70	0.0
17q11	rs241777	26633616	NOS2	C/T	0.75/0.72	0.75/0.72	0.76/0.73	0.75/0.73	1.20(1.10~1.30)	2.21×10^{-5}	0.93	0.0
17q21	rs62074054	45771816	NPEPPS-TBKBP1	C/T	0.65/0.62	0.62/0.61	0.65/0.59	0.63/0.60	1.16(1.08~1.25)	8.07×10^{-5}	0.42	0.0
Low-frequency variants												
1q23	rs2271966	160787900	ITLN1	A/G	0.05/0.05	0.04/0.03	0.06/0.04	0.04/0.02	1.49(1.22~1.82)	$4.73\times10^{-4*}$	0.83	0.0
3q22.3	rs16847421	137466335	NPM1P17	C/A	0.96/0.94	0.97/0.96	0.97/0.95	0.98/0.96	1.40(1.16~1.67)	$4.12\times10^{-5*}$	0.75	0.0
6q15	rs7760960	90311213	BACH2	T/C	0.05/0.04	0.05/0.03	0.05/0.04	0.04/0.03	1.45(1.20~1.75)	$4.36\times10^{-4*}$	0.40	0.0

A1:minor allele,A2:major allele.

*: Fisher's exact test

Supplementary Table 3B. The r² correlation and D' between 14 potential significant SNPs within reported loci and reported SNPs

Locus	Lead SNP	Position (Build 37)	Reported SNP	Position (Build 37)	r ² /D'
1p36	rs12030164	25166082	rs6600247	25305114	0.00/0.02
1q23	rs2271966	160787900	rs2039415	160854445	0.00/0.54
1q32	rs650854	210465315	rs12758027	210794808	0.00/0.09
2p15	rs13024541	62555737	rs10865331	62551472	1.00/1.00
2q11	rs2041751	102698360	rs4851529	102647300	0.00/0.07
2q11	rs2041751	102698360	rs2310173	102663628	-
2q11	rs2041751	102698360	rs2192752	102769373	0.03/0.77
2q33.2	rs12990568	204633655	rs11306716	204707771	-
2q37	rs10153794	241215701	rs4676410	241563739	0.00/0.03
3p24.1	rs3905899	28003439	rs10510607	28286261	0.00/0.04
3q22.3	rs16847421	137466335	rs6781808	137441372	0.00/0.14
5q15	rs17401719	96089046	rs30187	96124330	0.09/0.91
5q15	rs17401719	96089046	rs10045403	96147733	0.03/0.27
5q15	rs17401719	96089046	rs10050860	96122210	0.45/0.91
5q15	rs17401719	96089046	rs2910686	96252589	0.00/0.25
6q15	rs7760960	90311213	rs17765610	90665773	0.00/0.00
6q15	rs7760960	90311213	rs639575	90991131	0.00/0.04
6q27	rs86757	167507676	rs67025039	167415405	-
17q11	rs241777	26633616	rs2531875	26148167	0.00/0.09
17q11	rs241777	26633616	rs2297518	26096597	0.00/0.02
17q21	rs62074054	45771816	rs9901869	45575206	0.73/0.88
17q21	rs62074054	45771816	rs8070463	45768836	0.53/1.00

Supplementary Figure 5. The linkage disequilibrium haplotype blocks of 7 SNPs in ERAP1 region

(a) Location of 7 SNPs in ERAP1 region. One SNP(rs42398,OR=0.87,P=3.27×10-4) lied between exon 13 and exon 14, three SNPs located in the 6th,11th,12th exon of ERAP1: rs27434(OR=0.88, P=3.65×10-4), rs30187(OR=0.87, P=3.27×10-4),rs10050860 (OR=0.71, P=4.09×10-5). (b)SNPs exhibited strong linkage pattern are indicated by the black box, numbers in blocks represents the r² between SNPs and darker color of block indicates higher D' value.

